



SEQUENCE LISTING

<110> Yu et al.

<120> Methods of Treatment of Immune System Related Disorders
Using Neutrokine-alpha

<130> PF343P3C4

<150> 09/589,285

<151> 2000-06-08

<150> 09/507,968

<151> 2000-02-22

<150> 60/122,388

<151> 1999-03-02

<150> 60/124,097

<151> 1999-03-12

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<151> 1999-03-26

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<151> 1999-04-02

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<151> 1999-05-28

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<151> 1999-07-06

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<150> 60/176,015
<151> 2000-01-14

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<151> 1996-10-25

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<170> PatentIn Ver. 2.1

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ccaaccttca aagttcaagt agtgat atg gat gac tcc aca gaa agg gag cag 173
Met Asp Asp Ser Thr Glu Arg Glu Gln
1 5
tca cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag 221
Ser Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys
10 15 20 25
gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc 269
Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser
30 35 40
tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg 317
Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu
45 50 55
tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa 365
Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln
60 65 70
ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag 413
Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu
75 80 85
aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct 461
Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala

90	95	100	105	
cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga				509
Pro Ala Val Thr	Ala Gly Leu Lys Ile	Phe Glu Pro Pro	Ala Pro Gly	
	110	115	120	
gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt				557
Glu Gly Asn Ser Ser	Gln Asn Ser Arg Asn	Lys Arg Ala Val	Gln Gly	
	125	130	135	
cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt				605
Pro Glu Glu Thr Val Thr	Gln Asp Cys Leu Gln Leu	Ile Ala Asp Ser		
	140	145	150	
gaa aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt				653
Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr	Phe Val Pro Trp Leu			
	155	160	165	
ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata				701
Leu Ser Phe Lys Arg	Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile			
	170	175	180	185
ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat				749
Leu Val Lys Glu Thr Gly Tyr Phe Phe	Ile Tyr Gly Gln Val Leu Tyr			
	190	195	200	
act gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc				797
Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val				
	205	210	215	
cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att				845
His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile				
	220	225	230	
caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc				893
Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly				
	235	240	245	
att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga				941
Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg				
	250	255	260	265
gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca				989
Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala				
	270	275	280	
ttg aaa ctg ctg tgacctactt acaccatgtc ttagctatt ttctctcctt				1041
Leu Lys Leu Leu				
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 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 35 40 45
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 85 90 95
 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125
 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
 130 135 140
 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
 145 150 155 160
 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
 165 170 175
 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
 180 185 190
 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
 195 200 205
 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
 210 215 220
 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
 225 230 235 240
 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
 245 250 255
 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
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 275 280 285

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 35 40 45
 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60
 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65 70 75 80
 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 85 90 95
 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 100 105 110
 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 115 120 125
 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 130 135 140
 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 145 150 155 160
 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 165 170 175
 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 180 185 190
 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
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 Gln Val Tyr Phe Gly Ile Ile Ala Leu
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 35 40 45

Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
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 Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
 65 70 75 80
 Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
 85 90 95
 Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
 100 105 110
 Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
 115 120 125
 Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
 130 135 140
 His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
 145 150 155 160
 Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
 165 170 175
 Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
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 Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
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 Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
 35 40 45
 Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
 50 55 60
 Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
 65 70 75 80
 Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
 85 90 95
 Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
 100 105 110
 Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro

Sub
 C1
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115	120	125
Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg 130 135 140		
Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg 145 150 155 160		
Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu 165 170 175		
Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala 180 185 190		
Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly 195 200 205		
Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser 210 215 220		
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 a, t, g, or c

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Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
 35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
 50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
 85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
 100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
 115 120 125

c1
 cont

Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
 130 135 140
 Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
 145 150 155 160
 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
 165 170 175
 Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
 180 185 190
 Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
 195 200 205
 His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
 210 215 220
 Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
 225 230 235 240
 Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
 245 250 255
 Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
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 Gln Thr Phe Phe Gly Leu Tyr Lys Leu
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tcaaagttca agtagtgata tggatgactc cacagaaagg gagcagtcac gccttacttc 180
ttgccttaag aaaagagaag aaatgaaact gnaaggagtg tgtttccatc ctcccacgga 240
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 agtctggtga ctttgtttcg atgtattcaa aatatgcctg aaacactacc caataattcc 180
 tgctattcag ctggcattgc aaaactggna ggaaggagat gaactccaac ttgcaatacc 240
 aggggaaaaat gcacaattat cactgggatg gagatgttca catttttttg gtgccattga 300
 aactgctgtg acctncttac ancangtget gttingctatt ttncctncct nttctntggg 360
 aacctcttag gaaggaagga ttcttaactg ggaaataacc caaaaaaann ttaaangggg 420
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 ccgttcaggg tccagaagaa acagtcactc aagactgctt gcaactgntt gcagacagtg 180
 aaacaccaac tatacaaaaa ggctcccttc tgntgccaca tttgggcca ggaatggaga 240
 gatttcttcg tctggaaca ttttgccaaa ctcttcagat actcttttct ctctgggaat 300
 caaaggaaaa tctctactta gattnacaca tttgttccca tgggtntctt aagtttttaa 360
 aggggagtg ccttaggagg aaaaggggat aaatattggc caaggnactg gttantttnt 420
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C1
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ctggccagc 129

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 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1 5 10 15

aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96
 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
 20 25 30

cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 144
 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 35 40 45

gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60

tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 240
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80

gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 85 90 95

gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 336
 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110

aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 384
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125

agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac 432
 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
 130 135 140

aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa 480
 Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
 145 150 155 160

gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata 528

C1
 Cont

Glu	Lys	Glu	Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe	Ile		
				165					170					175			
tat	ggg	cag	gtt	tta	tat	act	gat	aag	acc	tac	gcc	atg	gga	cat	cta	576	
Tyr	Gly	Gln	Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His	Leu		
			180					185					190				
att	cag	agg	aag	aag	gtc	cat	gtc	ttt	ggg	gat	gaa	ttg	agt	ctg	gtg	624	
Ile	Gln	Arg	Lys	Lys	Val	His	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val		
			195				200					205					
act	ttg	ttt	cga	tgt	att	caa	aat	atg	cct	gaa	aca	cta	ccc	aat	aat	672	
Thr	Leu	Phe	Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn		
	210					215					220						
tcc	tgc	tat	tca	gct	ggc	att	gca	aaa	ctg	gaa	gaa	gga	gat	gaa	ctc	720	
Ser	Cys	Tyr	Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly	Asp	Glu	Leu		
225					230				235						240		
caa	ctt	gca	ata	cca	aga	gaa	aat	gca	caa	ata	tca	ctg	gat	gga	gat	768	
Gln	Leu	Ala	Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly	Asp		
				245				250						255			
gtc	aca	ttt	ttt	ggg	gca	ttg	aaa	ctg	ctg	tgacctactt	acaccatgctc					818	
Val	Thr	Phe	Phe	Gly	Ala	Leu	Lys	Leu	Leu								
			260				265										
tgtagctatt	ttcctccctt	tctctgtacc	tctaagaaga	aagaatctaa	ctgaaaatac	878											
caaaaaaaaa	aaaaaaaaaa	aaaaa				903											

<210> 19
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1 5 10 15
 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
 20 25 30
 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 35 40 45
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 85 90 95
 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn

115	120	125
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr		
130	135	140
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu		
145	150	155
Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile		
	165	170
Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu		
	180	185
Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val		
	195	200
Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn		
	210	215
Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu		
225	230	235
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp		
	245	250
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu		
	260	265

<210> 20
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 20
 His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp
 1 5 10 15
 Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg
 20 25 30
 Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val
 35 40 45
 Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met
 50 55 60
 Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe
 65 70 75 80
 Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
 85 90 95
 Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser
 100 105 110
 Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly
 115 120 125

Thr Phe Leu Gly Phe Val Lys Leu
130 135

<210> 21
<211> 462
<212> DNA
<213> Homo sapiens

<400> 21
atggctgttc aggggtccgga agaaaccggt actcaggact gccttcagct gatcgagac 60
tctgaaactc cgaccatcca gaaaggttct tacaccttggt ttccttggct gctttctttc 120
aaacgtgggt ctgccctgga agagaaagaa aacaaaatcc tggttaaaga aactgggttac 180
ttctttatct acggtcaggt tctttacact gataagacct acgccatggg tcacctgatt 240
cagcgtaaga aagttcacgt tttcggtgac gagctgtctc tggttactct gtttcgctgc 300
attcagaaca tgccggaaac tcttcctaac aactcctgct actctgctgg catcgcaaaa 360
ctggaagagg gtgatgaact gcagctggca attcctcgtg aaaacgcaca aatttctctg 420
gacggtgatg taaccttctt tgggtgcactg aaacttctgt aa 462

<210> 22
<211> 1040
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(468)

<400> 22
cgc gtg gta gac ctc tca gct cct cct gca cca tgc ctg cct gga tgc 48
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
1 5 10 15
cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act 96
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
20 25 30
tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg 144
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
35 40 45
gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc 192
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
50 55 60
atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat 240
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
65 70 75 80
gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg 288
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
85 90 95
gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac 336
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
100 105 110
aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag 384

C1
Cont

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
 115 120 125
 att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga 432
 Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130 135 140
 gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcaacttgct 478
 Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
 145 150 155
 ggagtgcgtg atcccccttcc ctctgtcttct ctgtacctcc gagggagaaa cagacgactg 538
 gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctctgtgaccc gttgaatctg 598
 atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658
 aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718
 acacgcaccg caaccttgct ttttgccttg ggtgacacat gttcagaatg cagggagatt 778
 tccttggtttt gcgatttgcc atgagaagag ggcccacaac tgcagggtcac tgaagcattc 838
 acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctctttttcca 898
 ggtaatacta tgggatacta tggaaagggtt gtttggtttt aaatctagaa gtcttgaact 958
 ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaagggttta 1018
 agtgtgaaaa aaaaaaaaaa aa 1040

<210> 23
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 23
 Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
 1 5 10 15
 Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
 20 25 30
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
 35 40 45
 Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50 55 60
 Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65 70 75 80
 Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 85 90 95
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
 100 105 110
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
 115 120 125
 Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130 135 140
 Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
 145 150 155

C1
 Cont

<210> 24
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> primer

 <400> 24
 ccaccagctc caggagaagg caactc

26

<210> 25
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <223> primer

<400> 25
 accgcgggac tgaaaatct

19

<210> 26
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <223> primer

<400> 26
 cacgcttatt tctgctgttc tga

23

<210> 27
 <211> 657
 <212> DNA
 <213> Homo sapiens

<400> 27
 taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagggccac 60
 cacgcggaga agctgccagc aagagcaaga gcccacaagg ccggtctggg ggaagctcca 120
 gctgtcaccg caggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
 cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
 ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttggt 300
 ccatggcttc tcagctttta aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
 gtcaaagaaa ctgggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420
 gccatgggac atctaattca gagggaaaaa gtccatgtct ttggggatga attgagctctg 480
 gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttctgtctat 540
 tcagctggca ttgcaaaact ggaagaagga gatgaacttc aacttgcaat accacgagaa 600
 aatgcacaaa tatcactgga tggagatgtc acattttttg gtgccctcaa actgctg 657

<210> 28
 <211> 219

<212> PRT
 <213> Homo sapiens

<400> 28

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15
 Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30
 Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60
 Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205
 Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 29

<211> 657

<212> DNA

<213> Homo sapiens

<400> 29

taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagagccac 60
 cacgcggaga agctgccagc aagagcaaga gcccccaagg ccggtctggg ggaagctcca 120
 gctgtcaccg cgggactgaa aatcttttgaa ccaccagctc caggagaagg caactccagt 180
 cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
 ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttggt 300
 ccatggcttc tcagctttta aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
 gtcaaagaaa ctggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420

C1
 Cont

gccatgggac atctaattca gaggaaaaaa gtccatgtct ttgggggatga attgagtctg 480
 gtgactttgt ttcgatgtat tcaaaatgat cctgaaacac tacccaataa ttcctgctat 540
 tcagctggca ttgcaaaact ggaagaagg gatgaacttc aacttgcaat accacgagaa 600
 aatgcacaaa taccactgga tggagatgtc acattttttg gtgccctcaa actgctg 657

<210> 30
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 30
 Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15
 Leu Gln Ser His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30
 Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60
 Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205
 Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 31
 <211> 38
 <212> DNA
 <213> Artificial Sequence

C1
 Cont

<220>
 <221> primer_bind
 <223> primer

 <400> 31
 ggtcgccggtt tctaacgcgg ccggttcaggg tccagaag 38

 <210> 32
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> primer

 <400> 32
 ctggttcggc ccaaggtacc aagcttgtac cttagatctt ttctagatc 49

 <210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> primer

 <400> 33
 ctggtagttc ttcggagtgt g 21

 <210> 34
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> primer

 <400> 34
 cgcgtagaa acggcgacc 19

 <210> 35
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> primer_bind
 <223> primer

 <220>
 <221> misc_feature
 <222> (7)
 <223> n equals deoxyinosine

C1
 Cont

<220>
 <221> misc_feature
 <222> (12)
 <223> n equals deoxyinosine

<220>
 <221> misc_feature
 <222> (16)
 <223> n equals deoxyinosine

<400> 35
 taccagntgg cngccttgca ag

22

<210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <223> primer

<220>
 <221> misc_feature
 <222> (3)
 <223> n equals deoxyinosine

<220>
 <221> misc_feature
 <222> (14)
 <223> n equals deoxyinosine

<220>
 <221> misc_feature
 <222> (16)..(17)
 <223> n equals deoxyinosine

<400> 36
 gtnacagcag tttanngca cc

22

<210> 37
 <211> 866
 <212> DNA
 <213> Mus musculus

<400> 37
 atggatgagt ctgcaaagac cctgccacca ccgtgcctct gtttttgctc cgagaaagga 60
 gaagatatga aagtgggata tgatcccatc actccgcaga aggaggaggg tgccctggttt 120
 gggatctgca gggatggaag gctgctggct gctaccctcc tgctggccct gttgtccagc 180
 agtttcacag cgatgtcctt gtaccagttg gctgccttgc aagcagacct gatgaacctg 240
 cgcatggagc tgcagagcta ccgaggttca gcaacaccag ccgccgcggg tgctccagag 300
 ttgaccgctg gagtcaaact cctgacaccg gcagctcctc gaccccacaa ctccagccgc 360
 ggccacagga acagacgcgc cttccaggga ccagaggaaa cagaacaaga tgtagacctc 420
 tcagctcctc ctgcaccatg cctgcctgga tgccgccatt ctcaacatga tgataatgga 480
 atgaacctca gaaacatcat tcaagactgt ctgcagctga ttgcagacag cgacacgccg 540
 gccttgagg agaaagagaa caaatagtg gtgaggcaaa caggctatct cttcatctac 600
 agccagggtc tatacacgga ccccatcttt gctatgggtc atgtcatcca gaggaagaaa 660

C1
 Cont

gtacacgtct ttggggacga gctgagcctg gtgaccctgt tccgatgtat tcagaatatg 720
 cccaaaacac tgcccaacaa ttcttgctac tcggctggca tcgcgaggct ggaagaagga 780
 gatgagattc agcttgcaat tcctcgggag aatgcacaga tttcacgcaa cggagacgac 840
 accttctttg gtgccctaaa actgct 866

<210> 38
 <211> 289
 <212> PRT
 <213> Mus musculus

<400> 38

Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
 1 5 10 15
 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
 20 25 30
 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
 35 40 45
 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
 50 55 60
 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 65 70 75 80
 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
 85 90 95
 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
 100 105 110
 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
 115 120 125
 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
 130 135 140
 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
 145 150 155 160
 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
 165 170 175
 Ser Asp Thr Pro Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg
 180 185 190
 Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro
 195 200 205
 Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe
 210 215 220
 Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met
 225 230 235 240
 Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg
 245 250 255

C1
 Cnt

Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala
260 265 270

Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu
275 280 285

Leu

<210> 39
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 39
cagactggat cgcgccaccat ggatgactcc acagaaag 38

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 40
cagactggta ccgtcctgcg tgcactacat ggc 33

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 41
tggtgtcttt ctaccaggtg g 21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 42
tttcttctgg accctgaacg g 21